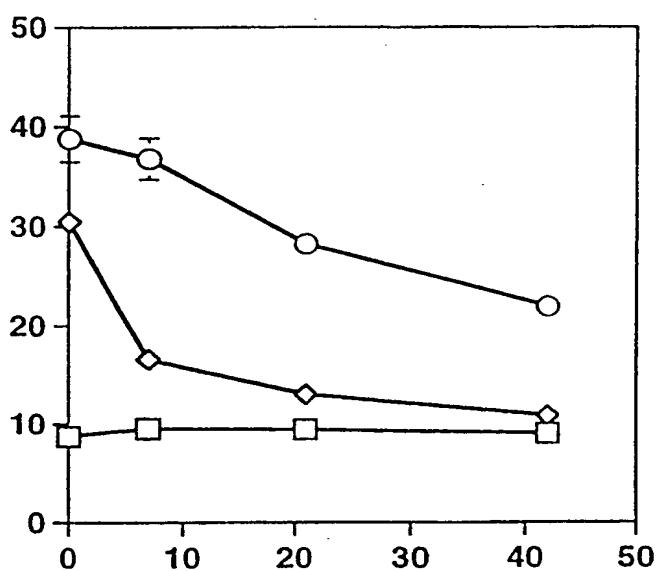


Figure 1



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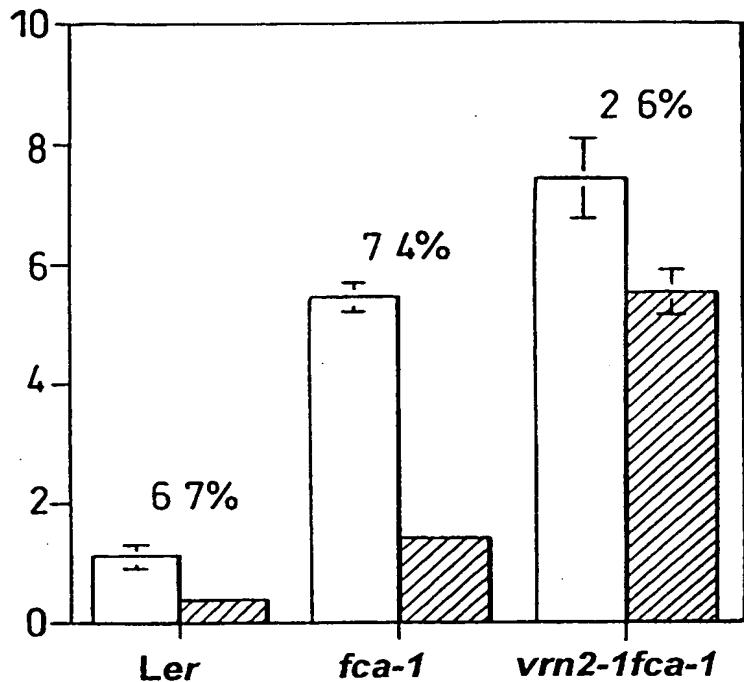
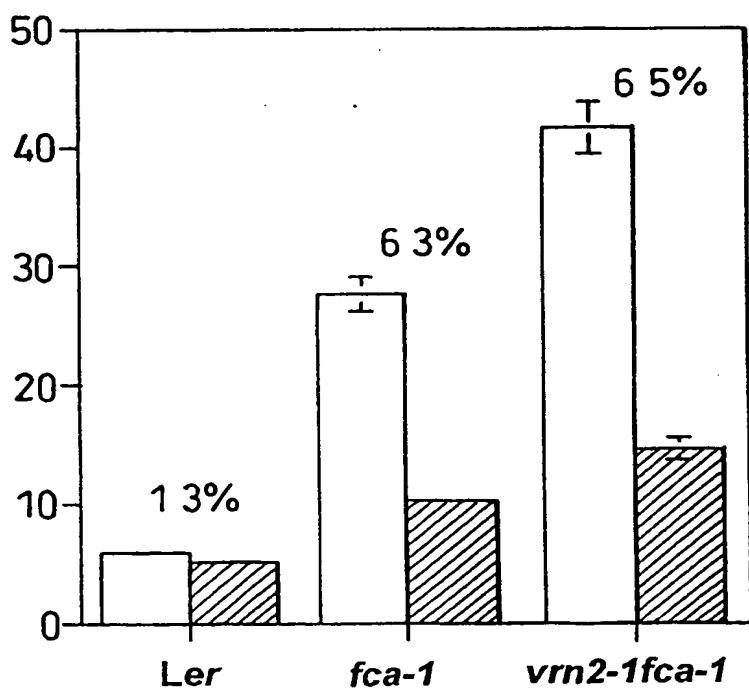
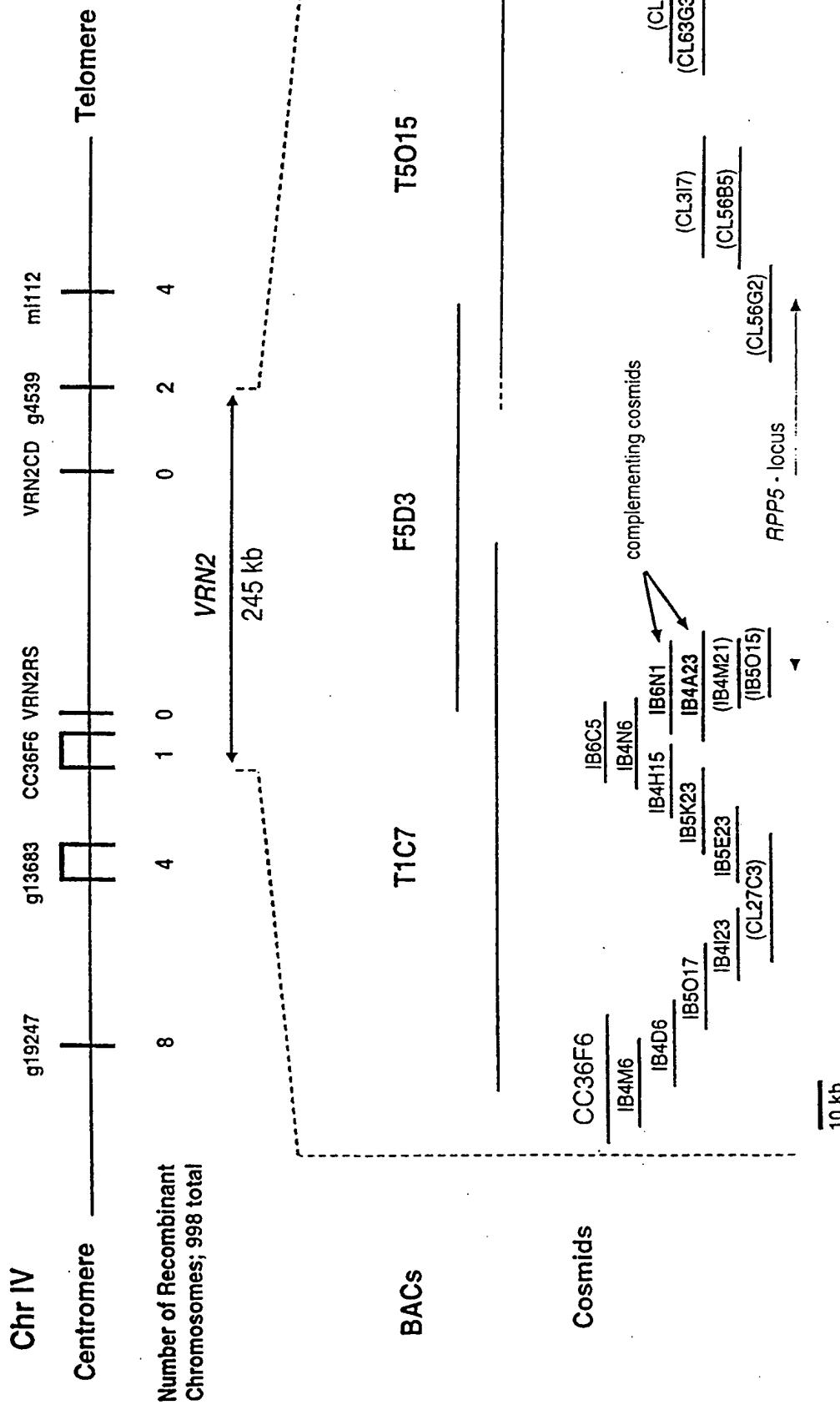
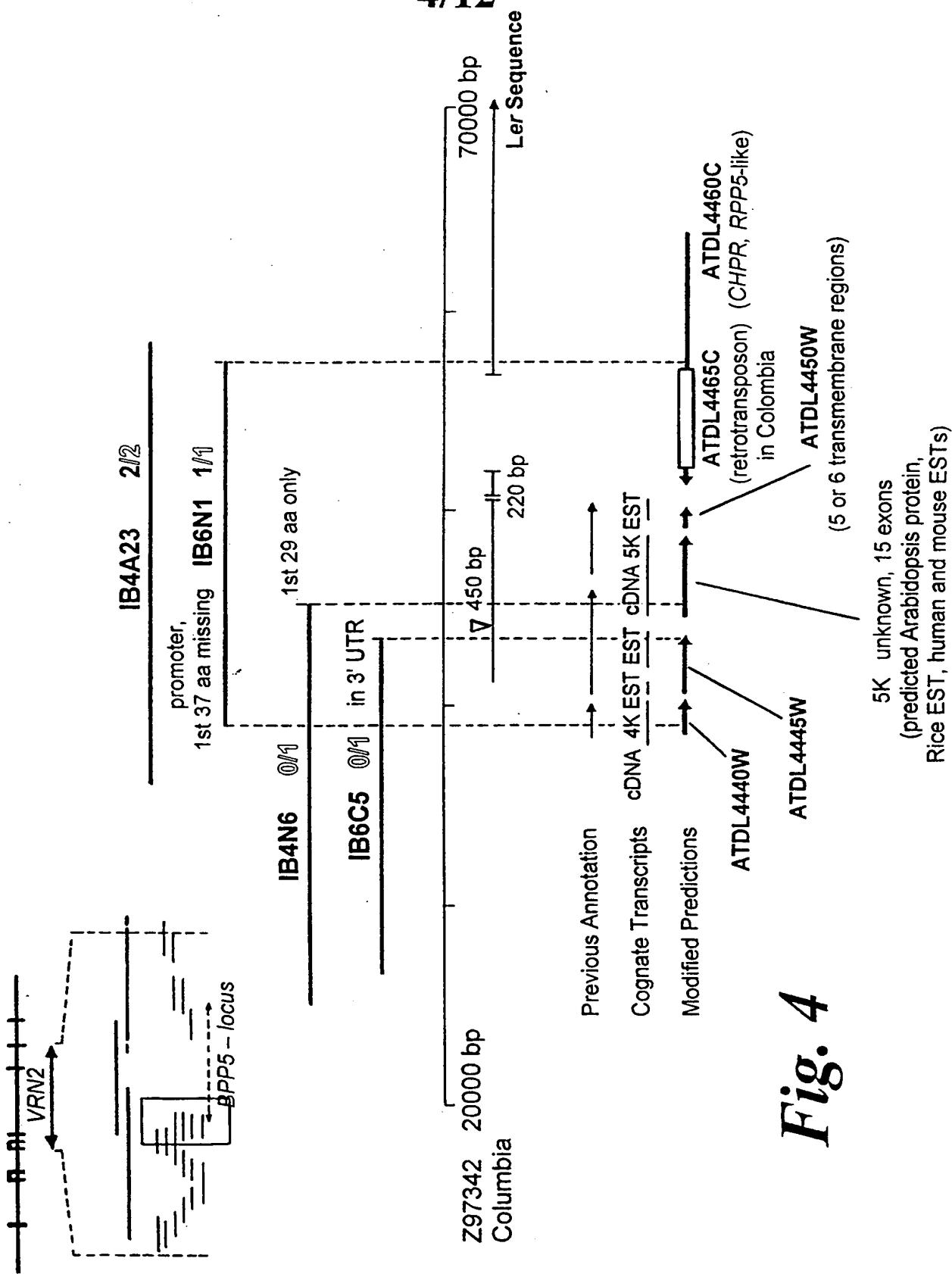
A*B**Fig. 2*

Figure 3

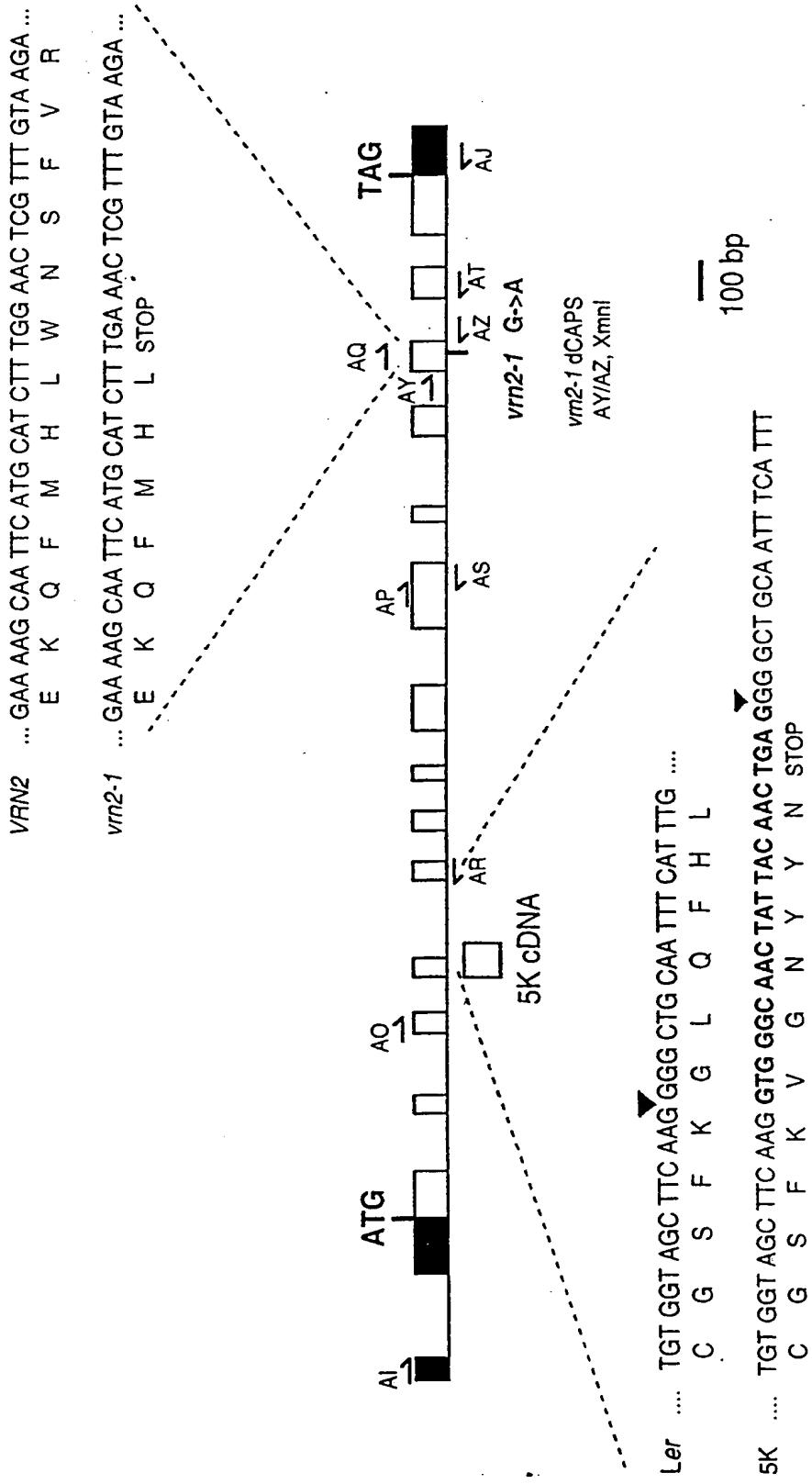


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Figure 5



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TTCTTCATA	TTTGCTTGCCTCTCTTACACAGCCAATCGGTGTTTGCAGCTTCAGGCC	CAATCCAAGACAT	5
TCTATATAAGC	ATTGCGAGAAGAGCGGGTCTAAATTGCTATGAGTTATCGCTATGACGTA	GGGAAATTCT	80
AATTAGGGAGCC	TCAGAGTTGACTAACCTCATATACTCATCGCTCTGACGTTGAGTGA	TTGAACAAGA	155
ATGTGTAGGC	CAGAATTGCGCGGAAATCCTCACCGGAGGAAGTGATTCAACTGATGAGA	ATCTTGATATAT	230
M C R Q N C R A K S S P E E V I S T D E N L L I Y			305
TGTAAACCTG	TTCGACTATATAACATCTTACCTTCGCTCTAGGCAACCCATGTTCT	CCAAGATGCTTG	25
C K P V R L Y N I F H L R S L G N P S F L P R C L			380
AACTACAAAATGGAGC	AAAGCGAAAAGAAAGTCAAGATCTACTGGGATGGTAGTTCAACTATAAGGAT	TTGT	50
N Y K I G A K R K R K S R S T G M V V F N Y K D C			455
AATAACACATTACAGAAA	ACTGAAGTTAGGGAGGATTGTTCTGTCATTTGCTATGCTATGTTAGCTTC		75
N N T L Q K T E V R E D C S C P F C S M L C G S F			530
AAGGGGCTG	CAATTTCATTTGAATTCTCATCTCATGATTATTGAGTTCAACGTTTCGAAGA	ATACCG	100
K G L Q F H L N S S H D L F E F E F K L F E E Y Q			605
ACAGTTAATGTTCTG	TTAAAACCTTAATTCTCATATTGAGGAAGAAGGAAAGTGATGACGATA	AAATTGAGGCC	125
T V N V S V K L N S F I F E E E G S D D D K F E P			680
TTCTCTCTCGCTG	CAAACCTCGTAAGCGGAGACAAAGAGGTGGCAGAAATAACACCAGGAG	ACTTAAAGTATGC	150
F S L C S K P R K R R Q R G G R N N T R R L K V C			755
TTTTTACCGTTGGATT	CACCCAGTTAACTAATGGCACAGAAAATGGAATCACCCACTTAATGATG	GGAAACCGT	175
F L P L D S P S L T N G T E N G I T L L N D G N R			830
GGTTTAGGATA	TCCCAGGGCACAGAGCTTGCTGGACAATTGAGATGACCAGCAACATT	CCACGCCATAGCC	200
G L G Y P E A T E L A G Q F E M T S N I P P A I A			905
CACTCTCTCTGGACGCTGGTGTAAAGTTATATGACAAGCGAAGCTGTGG	CTCCCTGCTACTAAAGACAAGAAAG	H S S L D A G A K V I L T S E A V V P A T K T R K	225
TTATCTGCTGAGC	GATCAGAGGCTAGAACGCCACCTACTTCTCAGAAACGCCATTCTATCATT	CTCACAGAGTC	980
L S A E R S E A R S H L L L Q K R Q F Y H S H R V			1055
CAGCCAAATGGCGCTT	GAGCAAGTAATGCTGACCGGGATAGCGAGGATGAAGTCGATGACGATGTG	CAGATTT	275
Q P M A L E O V M S D R D S E D E V D D D V A D F			1130
GAAGATGCCAGATG	CTGATGACTTTGGATGTGAATAAAGATGAAAAGCAATT	CATGCATCTTGGAACTCG	300
E D R Q M L D D F V D V N K D E K Q F M H L W N S			1205
TTTGTAAAGAAAACA	AAAGGGTTATAGCAGATGGTCATATCTCTGGCATGTGAACCAATTTC	CAAGATTTACCGAG	325
F V R K Q R V I A D G H I S W A C E A F S R F Y E			1280
AAAGAGTTGCACCG	TTACTCATCACCTCTGCTGGAGATTGTTGATTAAACTATGGAACCATGGACT	TT	350
K E L H R Y S S L F W C W R L F L I K L W N H G L			1355
GTCGACTCAGCCACC	ATCAACAACTGCAATACCACCTCGAGAATTGCCGTAATAGCTCAGACACCAC	ACCACC	375
V D S A T I N N C N T I L E N C R N S S D T T T T			1430
AACACAAACAACAGT	GTCGATCGTCCCAGTGACTCAAACACCAACAATAACATTGTTGATCAT	CCCAATGAC	400
N N N N S V D R P S D S N T N N N N I V D H P N D			1505
ATAAACAAACAAGAAC	AAATGTTGACAACAAGGACAATAACAGCAGAGACAAAGTAATTAA	AGGAAATCTCCGG	425
I N N K N N V D N K D N N S R D K V I K			1580
CTTTTATGATACCG	ATTATCGGATTGTAACTTATTCTCTTCTTAAAAAATTGTTAGGAGCA	AAACAAATT	445
TTATATGTTAGTGT	ATTCAACTGATTACATTAGTTAAAAAAATGGATTCTGCTATAACT		1655
			1722

Figure 6
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Figure 7

fca-1 W 323
 GAAAAGCAATTCATGCATCCTT TGG AACTCGTTTGTAAGAA
vrn2-1 TGA
 STOP

GAAAAGCAATTCATGCATCCTTGA~~AA~~ACTCGTTTGTAAGAA
 CTTNNNNNAAG
 Xmn I site

Diagnostic Primer: VRN2-AZ Antisense
 (contains a A and G mismatches at positions 5,7)

3' TGAGAAGACATTCTTTGTTCCATTGATGAAGAG 5'
 (CTT)NNNNA**G**
 Xmn I half-site

Upstream Primer: VRN2-AY 5' TGC GTT CATTAAAGTAGGCCAACAGAAAATGG 3'

Product: 170 bp PCR product for both *fca-1* and *vrn2-1*

PCR Products:

<i>fca-1</i>	GAAAAGCAATTCATGCATCCTTGA AA ACTCGTT <u>C</u> TGTAAGAA
<i>vrn2-1</i>	GAAAAGCAATTCATGGATCTT <u>G</u> AAACTCGTT <u>C</u> TGTAAGAA
Xmn I digest =>	<i>fca-1</i> no Xmn I site <i>vrn2-1</i> single Xmn I site
	170 bp 137 bp, 33 bp fragments

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Figure 8a

VRN2 Ler
AI163743 Prot
Rice C72616
AI Hyp 2245035
KIA00160

VRN2 Ler
AI163743 Prof
Rice C72616
AI Hyp 2245035
KIA00160

VRN2 Ler
AI163743 Prof
Rice C72616
AI Hyp 2245035
KIA00160

VRN2 Ler
AI163743 Prot
Rice C72616
AI Hyp 2245035
KIA00160

VRN2 Ler
AI163743 Prot
Rice C72616
AI Hyp 2245035
KIA00160

K	T	E	V	R	E	D	C	S	C	P	F	C	S	M	L	C	G	S	F	100
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
O	T	E	A	B	D	D	I	H	C	P	W	C	T	I	N	C	B	K	I	524

VfRN2 Ler
AI163743 Prot
Rice C72616
AI Hyp 2245035
KA00160

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Figure 8a continued

Figure 8a continued

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Figure 8a continued

	S	S	L	F	W	C	W	R	L	F	L	I	K	L	W	N	H	G	L	V
VRN2 Ler																				376
AI163743 Prot																				108
Rice C72616																				154
At Hyp 2245035																				141
KIA00160																				733
VRN2 Ler	L	S	L	D	L	C	W	R	Q	F	M	I	K	Q	W	D	Y	G	L	
AI163743 Prot	.	N	L	C	R	N	F	M	L	H	L	V	S	M	H	D	F	N	L	
Rice C72616																				
At Hyp 2245035	D	S	A	T	I	N	N	C	N	T	I	L	E	N	C	R	N	S	D	396
KIA00160																				108
VRN2 Ler	D	R	V	T	M	N	K	C	N	T	I	I	Y	H	N	I	S	T	T	
AI163743 Prot	S	I	M	S	I	D	K	A	V	T	K	L	R	R	E	M	Q	K	L	
Rice C72616																				154
At Hyp 2245035	T	T	T	N	N	N	S	V	D	R	P	S	D	S	N	T	N	N	753	
KIA00160																				161
VRN2 Ler	D	D	I	N	N	N	N	P	A	N	E	I	T	D	N	M	D	V	V	416
AI163743 Prot	K	G	E	S	A	S	N	P	T	R	T	T	D	E	I	E	T	E	D	108
Rice C72616																				154
At Hyp 2245035	D	D	I	N	N	N	N	P	A	N	E	I	T	D	N	M	D	V	V	181
KIA00160																				773
VRN2 Ler	N	N	I	V	D	H	P	N	D	I	N	N	K	N	N	V	D	N	K	436
AI163743 Prot																				108
Rice C72616	I	N	G	R	D	K	S	E	I	N	S	K	E	K	A	L	E	T	D	154
At Hyp 2245035																				186
KIA00160	N	N	S	R	D	K	V	I	K											793
VRN2 Ler	V	S	K	Q	S	K	K	Q	K	L										803
AI163743 Prot																				445
Rice C72616																				108
At Hyp 2245035																				154
KIA00160																				186

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111	57	85	69	59	65	29	244
							82
							832
							100
							269
							610
							366
							590
							2734
							420
							405
							271

The sequence logo displays the conservation of amino acids across various species. The columns represent positions in the sequence, and the rows represent amino acids. The height of each bar indicates the frequency of that amino acid at that position. A black background is used for the bars.

Figure 8b

VRN2 Ler
 At D119 S51478
 At D119 S51478
 At SUP U38946
 At Hyp 2191171
 At Hyp 3377806
 Sc Pep7 91500
 Sc TFIIA 730931
 Sp Hyp 1351713
 Ce Hyp 255942
 Ce Hyp 2854197
 Ce Hyp 304459
 Dm BRCORE-NS-Z3
 Dm GAGA 729556
 Dm ken 3550814
 Hs ATBF-1 976347
 Hs KIA00160
 Hs ZNF142 3123312
 Mm FOG 2252814
 Mm Spail 1296645
 Rn Roaz 2149792
 Xm ZF1 532083